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NEWS 15	DEC 22	Value-Added Indexing Improves Access to World Traditional Medicine Patents in CAplus
NEWS 16	JAN 24	The new and enhanced DPCI file on STN has been released
NEWS 17	JAN 26	Improved Timeliness of CAS Indexing Adds Value to USPATFULL and USPAT2 Chemistry Patents
NEWS 18	JAN 26	Updated MeSH vocabulary, new structured abstracts, and other enhancements improve searching in STN reload of MEDLINE
NEWS 19	JAN 28	CABA will be updated weekly
NEWS 20	FEB 23	PCTFULL file on STN completely reloaded
NEWS 21	FEB 23	STN AnaVist Test Projects Now Available for Qualified Customers
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Thomas S Heard Ph.,D.

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DICTIONARY FILE UPDATES: 16 MAR 2011 HIGHEST RN 1268669-05-1

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=> S ETC.{4,20}CTK/SQSP
L1 161 ETC.{4,20}CTK/SQSP

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=> FIL HCAP
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    36.35      36.58

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FILE COVERS 1907 - 17 Mar 2011  VOL 154 ISS 12
FILE LAST UPDATED: 16 Mar 2011  (20110316/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Dec 2010
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Dec 2010

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=> L1
L2          65 L1

=> L2 AND (PD<20031115)
      23962069 PD<20031115
                    (PD<20031115)
L3          26 L2 AND (PD<20031115)

=> D L3 IBIB ABS HITSTR 1-26

L3   ANSWER 1 OF 26  HCAPLUS  COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER:         2006:693209  HCAPLUS
DOCUMENT NUMBER:          145:138709
TITLE:                    Class BI and CI scavenger receptors cloned from
                          Chinese hamster and Drosophila melanogaster and their
                          specificity for low-density lipoproteins and modified
                          low-density lipoproteins
INVENTOR(S):              Krieger, Monty; Acton, Susan L.
PATENT ASSIGNEE(S):       Massachusetts Institute of Technology, USA
SOURCE:                   U.S., 42 pp., Cont.-in-part of U.S. Ser. 265,428.
                          CODEN: USXXAM
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DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 7078511	B1	20060718	US 1997-765108	19970327
US 6429289	B1	20020806	US 1994-265428	19940623 <--
WO 9600288	A2	19960104	WO 1995-US7721	19950619 <--
WO 9600288	A3	19960404		
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TT, UA, US, UZ, VN				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6350859	B1	20020226	US 1999-241581	19990202 <--
US 20050136005	A1	20050623	US 2004-933037	20040902

PRIORITY APPLN. INFO.: US 1994-265428 A2 19940623
WO 1995-US7721 W 19950619
US 1996-749907 A3 19961115
US 1997-765108 A3 19970327
US 1999-385799 A1 19990830

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB Two distinct scavenger receptor (SR) type proteins having high affinity for modified lipoproteins and other ligands were isolated, characterized, and cloned. SR-BI, an Ac-LDL and LDL binding scavenger receptor, which is distinct from the type I and type II macrophage scavenger receptors, was isolated and characterized and cDNA encoding the receptor cloned from a variant of Chinese hamster ovary cells, designated Var-261. SR-CI, a non-mammalian Ac-LDL binding scavenger receptor having high ligand affinity and broad specificity, was isolated from Drosophila melanogaster. The isolated receptors are useful in screening for drugs that inhibit uptake of cholesterol in endothelial or adipose cells or macrophages, resp. They are also useful as probes for the isolation of other lipoprotein receptors and in research the roles of these receptors.

IT 899454-75-2
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; class BI and CI scavenger receptors cloned from Chinese hamster and Drosophila melanogaster and their specificity for low-d. lipoproteins and modified low-d. lipoproteins)

RN 899454-75-2 HCAPLUS
CN Scavenger receptor SR-CI (Drosophila melanogaster) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
REFERENCE COUNT: 98 THERE ARE 98 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2003:799440 HCAPLUS
DOCUMENT NUMBER: 140:25694
TITLE: Natural selection drives Drosophila immune system evolution

AUTHOR(S): Schlenke, Todd A.; Begun, David J.
CORPORATE SOURCE: Section of Evolution and Ecology, Division of Biological Sciences, University of California, Davis, CA, 95616, USA
SOURCE: Genetics (2003), 164(4), 1471-1480
CODEN: GENTAE; ISSN: 0016-6731
PUBLISHER: Genetics Society of America
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Evidence from disparate sources suggests that natural selection may often play a role in the evolution of host immune system proteins. However, there have been few attempts to make general population genetic inferences on the basis of anal. of several immune-system-related genes from a single species. Here we present DNA polymorphism and divergence data from 34 genes thought to function in the innate immune system of D. simulans and compare these data to those from 28 non-immunity genes sequenced from the same lines. Several statistics, including average KA/KS ratio, average silent heterozygosity, and average haplotype diversity, significantly differ between the immunity and non-immunity genes, suggesting an important role for directional selection in immune system protein evolution. In contrast to data from mammalian Igs and other proteins, we find no strong evidence for the selective maintenance of protein diversity in Drosophila immune system proteins. This may be a consequence of Drosophila's generalized innate immune response.
IT 579431-07-5, Sr-CI (Drosophila simulans strain Sim1)
579431-09-7, Sr-CI (Drosophila simulans strain Sim2)
579431-11-1, Sr-CI (Drosophila simulans strain Sim3)
579431-13-3, Sr-CI (Drosophila simulans strain Sim4)
579431-15-5, Sr-CI (Drosophila simulans strain Sim5)
579431-17-7, Sr-CI (Drosophila simulans strain Sim6)
579431-19-9, Sr-CI (Drosophila simulans strain Sim7)
579431-21-3, Sr-CI (Drosophila simulans strain Sim8)
586329-23-9 586329-25-1 586329-27-3
586329-29-5 586329-31-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; natural selection drives Drosophila immune system evolution)
RN 579431-07-5 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim1) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-09-7 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim2) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-11-1 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim3) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-13-3 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim4) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-15-5 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim5) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-17-7 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim6) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-19-9 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim7) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 579431-21-3 HCAPLUS
CN Sr-CI (Drosophila simulans strain Sim8) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 586329-23-9 HCAPLUS
CN Sr-CI (Drosophila melanogaster strain Mel1) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 586329-25-1 HCAPLUS
CN Sr-CI (Drosophila melanogaster strain Mel2) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 586329-27-3 HCAPLUS
CN Sr-CI (Drosophila melanogaster strain Mel3) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 586329-29-5 HCAPLUS
CN Sr-CI (Drosophila melanogaster strain Mel4) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 586329-31-9 HCAPLUS
CN Sr-CI (Drosophila melanogaster strain Mel5) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT: 80 THERE ARE 80 CAPLUS RECORDS THAT CITE THIS RECORD (80 CITINGS)
REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2003:765150 HCAPLUS
DOCUMENT NUMBER: 139:241381
TITLE: Expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins
INVENTOR(S): Tanaka, Hiroaki; Dumas Milne, Edwards Jean-Baptiste; Giordano, Jean-Yves; Jobert, Severin; Bejanin, Stephane
PATENT ASSIGNEE(S): Genset, Fr.
SOURCE: Can. Pat. Appl., 163 pp.
CODEN: CPXXEB
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 13
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

CA 2343602	A1	20011018	CA 2001-2343602	20010417 <--
CA 2343602	A1	20011018	CA 2001-2343602	20010417 <--
PRIORITY APPLN. INFO.:			US 2000-197873P	P 20000418
			CA 2001-2343602	20010417

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from cDNA libraries derived from mRNAs having intact 5' ends are disclosed. The 5' ESTs and consensus contigated 5' ESTs may be used to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstract record is one of thirteen records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 599392-56-0
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins)

RN 599392-56-0 HCAPLUS

CN Secretory protein (human clone CA2343602-SEQID-18450 precursor) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 2003:571103 HCAPLUS
DOCUMENT NUMBER: 139:122690
TITLE: Albumin fusion proteins for prolonged shelf-life of therapeutic proteins
INVENTOR(S): Ballance, David James; Turner, Andrew John; Rosen, Craig A.; Haseltine, William A.
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA; Delta Biotechnology Limited; Principia Pharmaceutical Corporation
SOURCE: PCT Int. Appl., 598 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 12
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003060071	A2	20030724	WO 2002-US40891	20021223 <--
WO 2003060071	A3	20040226		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ,

CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA	2471363	A1	20030724	CA 2002-2471363	20021223 <--
AU	2002364586	A1	20030730	AU 2002-364586	20021223 <--
EP	1463751	A2	20041006	EP 2002-799966	20021223
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
JP	2005514060	T	20050519	JP 2003-560158	20021223
EP	1997829	A1	20081203	EP 2008-75724	20021223
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, SI, SK, TR				
EP	2261250	A1	20101215	EP 2010-75030	20021223
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, SI, SK, TR				
EP	2277888	A2	20110126	EP 2010-75454	20021223
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EP	2277889	A2	20110126	EP 2010-75466	20021223
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, SI, SK, TR				
EP	2277910	A1	20110126	EP 2010-75467	20021223
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, SI, SK, TR				
US	20050186664	A1	20050825	US 2004-775204	20040211
US	7141547	B2	20061128		
JP	2006176514	A	20060706	JP 2005-365640	20051219
US	20060194735	A1	20060831	US 2006-429276	20060508
US	7592010	B2	20090922		
US	20060276396	A1	20061207	US 2006-429373	20060508
US	7238667	B2	20070703		
US	20080213886	A1	20080904	US 2006-429374	20060508
US	7847079	B2	20101207		
US	20080004206	A1	20080103	US 2006-495624	20060731
US	20070244047	A1	20071018	US 2007-714841	20070307
US	20070259815	A1	20071108	US 2007-783419	20070409
US	20080146503	A1	20080619	US 2007-772643	20070702
US	7799759	B2	20100921		
US	20080153751	A1	20080626	US 2007-929828	20071030
US	20080161243	A1	20080703	US 2007-929714	20071030
US	20080167238	A1	20080710	US 2007-929912	20071030
US	20080167239	A1	20080710	US 2007-929939	20071030
US	20080167240	A1	20080710	US 2007-929953	20071030
US	20090093402	A1	20090409	US 2007-929702	20071030
US	20090099073	A1	20090416	US 2007-929946	20071030
US	20080194481	A1	20080814	US 2007-932823	20071031
JP	2009213477	A	20090924	JP 2009-109615	20090428
US	20100291033	A1	20101118	US 2010-793652	20100603
US	20110002888	A1	20110106	US 2010-793658	20100603
US	20110009312	A1	20110113	US 2010-836447	20100714
JP	2011015690	A	20110127	JP 2010-185419	20100820

PRIORITY APPLN. INFO.:

US 2001-341811P	P	20011221
US 2002-350358P	P	20020124
US 2002-351360P	P	20020128
US 2002-359370P	P	20020226
US 2002-360000P	P	20020228
US 2002-367500P	P	20020327
US 2002-370227P	P	20020408
US 2002-378950P	P	20020510

US 2002-382617P	P	20020524
US 2002-383123P	P	20020528
US 2002-385708P	P	20020605
US 2002-394625P	P	20020710
US 2002-398008P	P	20020724
US 2002-402131P	P	20020809
US 2002-402708P	P	20020813
US 2002-411355P	P	20020918
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US 2002-414984P	P	20021002
US 2002-417611P	P	20021011
US 2002-420246P	P	20021023
US 2002-423623P	P	20021105
EP 2002-799966	A3	20021223
EP 2008-75724	A3	20021223
EP 2010-75030	A3	20021223
JP 2003-560158	A3	20021223
WO 2002-US40891	W	20021223
US 2003-441305P	P	20030122
US 2003-453201P	P	20030311
US 2003-467222P	P	20030502
US 2003-472816P	P	20030523
US 2003-476267P	P	20030606
US 2003-505172P	P	20030924
US 2003-506746P	P	20030930
WO 2004-US1369	A1	20040120
US 2004-542274P	P	20040209
US 2004-775204	A1	20040211
US 2004-549901P	P	20040305
US 2004-556906P	P	20040329
US 2004-636603P	P	20041217
WO 2005-US4041	A2	20050209
US 2005-175690	A2	20050707
US 2005-707521P	P	20050812
US 2005-712386P	P	20050831
US 2005-732724P	P	20051103
US 2006-776914P	P	20060228
US 2006-781361P	P	20060313
US 2006-429276	A2	20060508
US 2006-429373	A3	20060508
US 2006-810182P	P	20060602
US 2006-813682P	P	20060615
US 2006-495624	A2	20060731
US 2006-500508	A3	20060808
US 2007-714841	A2	20070307
US 2007-783419	B1	20070409
US 2007-929714	A2	20071030
US 2007-932823	A3	20071031
US 2009-426882	A2	20090420
US 2009-534585	A2	20090803

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention encompasses albumin fusion proteins. Many therapeutic proteins in their native state or when recombinantly produced are typically labile mols. exhibiting short shelf-lives, particularly when formulated in aqueous solns.; fusions of the therapeutic protein with human serum albumin have a longer serum half-life and/or stabilized activity in solution (or in a pharmaceutical composition) in vitro and/or in vivo than the

corresponding unfused therapeutic mols. Thus, albumin fusion proteins are provided comprising granulocyte colony-stimulating factor, interleukin 2, parathormone, erythropoietin, interferon β, interferon α2, interferon A/D hybrid, a single-chain insulin analog, growth hormone, and (7-36)GLP-1. Nucleic acid mols. encoding the albumin fusion proteins of the invention are also encompassed by the invention, as are vectors containing these nucleic acids, host cells transformed with these nucleic acids vectors, and methods of making the albumin fusion proteins of the invention and using these nucleic acids, vectors, and/or host cells. Addnl. the present invention encompasses pharmaceutical compns. comprising albumin fusion proteins and methods of treating or preventing diseases, disorders or conditions related to diabetes mellitus using albumin fusion proteins of the invention.

IT 562127-68-8
RL: PRP (Properties)
(unclaimed protein sequence; albumin fusion proteins for prolonged shelf-life of therapeutic proteins)

RN 562127-68-8 HCAPLUS

CN 359: PN: WO03060071 SEQID: 334 unclaimed protein (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L3 ANSWER 5 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 2003:539800 HCAPLUS

DOCUMENT NUMBER: 139:64475

TITLE: Abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant

INVENTOR(S): Kreps, Joel; Briggs, Steven P.; Cooper, Bret; Glazebrook, Jane; Goff, Stephen A.; Katagiri, Fumiyaki; Moughamer, Todd; Provart, Nicholas; Ricke, Darrell; Zhu, Tong

PATENT ASSIGNEE(S): Syngenta Participations AG, Switz.

SOURCE: PCT Int. Appl., 177 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 11

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008540	A2	20030130	WO 2002-XA19668	20020621 <--
WO 2003008540	A3	20031204		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2003008540	A2	20030130	WO 2002-US19668	20020621 <--

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     WO 2003008540        A3    20031204
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              CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
              GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
              LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
              PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
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     EP 1925672           A1    20080528    EP 2008-102091          20020621
          R:  AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC,
              NL, PT, SE, TR
     US 20030135888       A1    20030717    US 2002-259165          20020926 <--
     US 20040010815       A1    20040115    US 2002-259194          20020926
PRIORITY APPLN. INFO.:                       US 2001-300112P      P  20010622
                                             US 2001-314662P      P  20010824
                                             US 2001-325277P      P  20010926
                                             US 2001-332132P      P  20011121
                                             WO 2002-US19668         20020621
                                             US 2002-368327P      P  20020327
                                             US 2002-370620P      P  20020404
                                             US 2002-370743P      P  20020404
                                             EP 2002-775690       A3 20020621
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB   Abiotic stress responsive polynucleotides and polypeptides are disclosed.
     Also disclosed are vectors, expression cassettes, host cells, and plants
     containing such polynucleotides. Also provided are methods for using such
     polynucleotides and polypeptides, for example, to alter the responsiveness
     of a plant to abiotic stress. Rice (Oryza sativa japonica) cDNA library
     was constructed and sequenced, and used in GeneChip standard protocol for
     expression profiling of stress-regulated genes. Based on the profiles,
     clusters of nucleic sequences that were altered at least two-fold in
     response to the stress condition were identified. Identification of
     abiotic stress responsive genes using yeast two hybrid system was also
     demonstrated. Rice orthologs of Arabidopsis abiotic stress genes were
     identified by reverse genetics. Transgenic rice expressing "abiotic
     stress candidate gene" was produced. The present invention claimed
     abiotic stress responsive cDNAs (SEQ IDs 1-4131, 8263-8353, 8445-8829 and
     17505-17506) and proteins (SEQ IDs 4132-8262, 8354-8444, and 8830-9214),
     but the Sequence Listing was not made available on publication of the
     patent application.
IT   549579-05-7
     RL: PRP (Properties)
        (unclaimed protein sequence; abiotic stress responsive polynucleotides
        and polypeptides from plants and methods of altering the stress
        responsiveness of a plant)
RN   549579-05-7  HCAPLUS
CN   979: PN: WO03008540 SEQID: 6823 unclaimed protein (9CI)  (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT:     5     THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD
                               (5 CITINGS)

L3   ANSWER 6 OF 26  HCAPLUS  COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER:         2003:253983  HCAPLUS
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DOCUMENT NUMBER: 139:18104
TITLE: What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence
AUTHOR(S): Mannhaupt, Gertrud; Montrone, Corinna; Haase, Dirk; Mewes, H. Werner; Aign, Verena; Hoheisel, Joerg D.; Fartmann, Berthold; Nyakatura, Gerald; Kempken, Frank; Maier, Josef; Schulte, Ulrich
CORPORATE SOURCE: Department of Genome Oriented Bioinformatics, Technical University of Munich, Freising-Weihenstephan, Germany
SOURCE: Nucleic Acids Research (2003), 31(7), 1944-1954 CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The German Neurospora Genome Project has assembled sequences from ordered cosmid and BAC clones of linkage groups II and V of the genome of Neurospora crassa in 13 and 12 contigs, resp. Including addnl. sequences located on other linkage groups a total of 12 Mb were subjected to a manual gene extraction and annotation process. The genome comprises a small number of repetitive elements, a low degree of segmental duplications and very few paralogous genes. The anal. of the 3218 identified open reading frames provides a first overview of the protein equipment of a filamentous fungus. Significantly, N. crassa possesses a large variety of metabolic enzymes including a substantial number of enzymes involved in the degradation of complex substrates as well as secondary metabolism While several of these enzymes are specific for filamentous fungi many are shared exclusively with prokaryotes. Sequences predicted genes and anal. results are accessible online at http://mips.gsf.de/proj/neurospora/.

IT 486687-40-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Neurospora crassa)

RN 486687-40-5 HCAPLUS
CN Protein (Neurospora crassa gene B9B15.005) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 35 THERE ARE 35 CAPLUS RECORDS THAT CITE THIS RECORD (35 CITINGS)
REFERENCE COUNT: 94 THERE ARE 94 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2003:112150 HCAPLUS
DOCUMENT NUMBER: 138:131969
TITLE: Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
AUTHOR(S): Strausberg, Robert L.; Feingold, Elise A.; Grouse, Lynette H.; Derge, Jeffery G.; Klausner, Richard D.; Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn M.; Schuler, Gregory D.; Altschul, Stephen F.; Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather; Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh, Florence; Diatchenko, Luda; Marusina, Kate; Farmer, Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton,

Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant, Tom L.; Scheetz, Todd E.; Brownstein, Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero; Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.; Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan, Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.; Richards, Stephen; Worley, Kim C.; Hale, Sarah; Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.; Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica; Helton, Erin; Ketteman, Mark; Madan, Anuradha; Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle; Madan, Anup; Young, Alice C.; Shevchenko, Yuriy; Bouffard, Gerard G.; Blakesley, Robert W.; Touchman, Jeffrey W.; Green, Eric D.; Dickson, Mark C.; Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy; Myers, Richard M.; Butterfield, Yaron S. N.; Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones, Steven J. M.; Marra, Marco A.
CORPORATE SOURCE: National Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The National Institutes of Health Mammalian Gene Collection (MGC) Program is a multiinstitutional effort to identify and sequence a cDNA clone containing a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstract record is one of eleven records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT 479954-88-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)
RN 479954-88-6 HCAPLUS
CN Similar to tigger transposable element derived 4 (human clone MGC:43837 IMAGE:5273281) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 8 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2003:8423 HCAPLUS
DOCUMENT NUMBER: 138:118304
TITLE: Analysis of the mouse transcriptome based on

functional annotation of 60,770 full-length cDNAs

AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SOURCE: Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts,

79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstract record is one of thirty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 485744-36-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

RN 485744-36-3 HCAPLUS

CN Protein (mouse strain C57BL/6J clone C230077C14 597-amino acid) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 2003:7639 HCAPLUS

DOCUMENT NUMBER: 138:131941

TITLE: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.;

Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SOURCE: Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstract record is one of thirty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 484581-01-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

RN 484581-01-3 HCAPLUS

CN Protein (mouse strain C57BL/6J clone A230102I24 585-amino acid) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 10 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 2003:6106 HCAPLUS

DOCUMENT NUMBER: 138:67938

TITLE: Defensin polynucleotides from plants and methods of their use as pesticides and for modulating development and defense responses

INVENTOR(S): Cahoon, Rebecca E.; Herrmann, Rafael; Harvell, Leslie T.; Lu, Albert Laurence; McCutchen, Billy Fred; Navarro Acevedo, Pedro A.; Simmons, Carl R.; Wong, James F. H.

PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., USA; E. I. Du

Pont de Nemours &
Co.
SOURCE: PCT Int. Appl., 307 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003000863	A2	20030103	WO 2002-US21177	20020621 <--
WO 2003000863	A3	20051020		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, AP, EA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, EP, OA				
MX 2003011890	A	20040603	MX 2003-11890	19981113
CA 2451517	A1	20030103	CA 2002-2451517	20020621 <--
CA 2724158	A1	20030103	CA 2002-2724158	20020621 <--
CA 2724166	A1	20030103	CA 2002-2724166	20020621 <--
CA 2724187	A1	20030103	CA 2002-2724187	20020621 <--
CA 2724188	A1	20030103	CA 2002-2724188	20020621 <--
CA 2724313	A1	20030103	CA 2002-2724313	20020621 <--
CA 2724316	A1	20030103	CA 2002-2724316	20020621 <--
AU 2002322388	A1	20030108	AU 2002-322388	20020621 <--
US 20030041348	A1	20030227	US 2002-178213	20020621 <--
US 6911577	B2	20050628		
EP 1572880	A2	20050914	EP 2002-756376	20020621
EP 1572880	A3	20051207		
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BR 2002010593	A	20070102	BR 2002-10593	20020621
EP 2270184	A2	20110105	EP 2010-10407	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				
EP 2270185	A2	20110105	EP 2010-10408	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				
EP 2270186	A2	20110105	EP 2010-10409	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				
EP 2270187	A2	20110105	EP 2010-10641	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				
EP 2270165	A2	20110105	EP 2010-10642	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				
EP 2270188	A2	20110105	EP 2010-10644	20020621
R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE, TR				

US 20050273881	A1	20051208	US 2005-123896		20050506
US 7396980	B2	20080708			
US 20090025103	A1	20090122	US 2008-132492		20080603
US 7897847	B2	20110301			
US 20090031448	A1	20090129	US 2008-132442		20080603
US 7855327	B2	20101221			
US 20090031449	A1	20090129	US 2008-132529		20080603
US 20090077688	A1	20090319	US 2008-132478		20080603
US 7855328	B2	20101221			
US 20090077689	A1	20090319	US 2008-132513		20080603
US 20090077690	A1	20090319	US 2008-132536		20080603
PRIORITY APPLN. INFO.:			US 2001-300152P	P	20010622
			US 2001-300241P	P	20010622
			CA 2002-2451517	A3	20020621
			EP 2002-756376	A3	20020621
			US 2002-178213	A3	20020621
			WO 2002-US21177	W	20020621
			US 2005-123896	A3	20050506

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB Methods and compns. for modulating development and defense responses are provided. Particularly, isolated nucleic acids having nucleotide and encoded amino acid sequences for defensins from plants are provided. The nucleotide sequences of the invention encode small cysteine-rich proteins and are variously annotated or described as defensins, defensin-like proteins, antimicrobial peptides, anti-pathogenic peptides, thionins, antifungal peptides, protease inhibitors, amylase inhibitors, scorpion toxin-like proteins, and small cysteine-rich proteins. They are referred to as defensins as they exhibit similarity in primary structure to insect defensins. The sequences can be used in expression cassettes for modulating development, developmental pathways, and defense responses. Transformed plants, plant cells, tissues, and seed are also provided.

IT 479764-81-3 479764-82-4 479764-84-6
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; defensin polynucleotides from plants and methods of their use as pesticides and for modulating development and defense responses)

RN 479764-81-3 HCAPLUS
CN Defensin (Momordica charantia clone CS104 sequence homolog precursor) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 479764-82-4 HCAPLUS
CN Defensin (Momordica charantia clone CS104 sequence homolog) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 479764-84-6 HCAPLUS
CN Defensin (Momordica charantia clone CS105 sequence homolog precursor) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 11 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2002:964378 HCAPLUS

DOCUMENT NUMBER: 138:36239
TITLE: Non-endogenous, constitutively activated plant G protein-coupled receptor GCR1 for modulation of plant development
INVENTOR(S): Colucci, Gabriella
PATENT ASSIGNEE(S): Arena Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002100882	A2	20021219	WO 2002-US17809	20020605 <--
WO 2002100882	A3	20030410		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2449553	A1	20021219	CA 2002-2449553	20020605 <--
AU 2002310326	A1	20021223	AU 2002-310326	20020605 <--
US 20030073812	A1	20030417	US 2002-164163	20020605 <--
EP 1404708	A2	20040407	EP 2002-737396	20020605
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.:		
US 2001-295948P	P	20010605
US 2001-308267P	P	20010726
US 2001-330363P	P	20011018
US 2001-339281P	P	20011211
US 2002-372131P	P	20020412
WO 2002-US17809	W	20020605

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The invention relates to transmembrane receptors for which the endogenous ligand has not been identified, and specifically to a plant GPCR ("GCR1") that has been altered to establish constitutive activity of the receptor. In some embodiments, the altered versions of GCR1 are used for the direct identification of candidate compds. as receptor agonists, inverse agonists or partial agonists for use in, for example and not limitation, herbicidal relevance; germination; growth elongation; seed dormancy; and fruit and vegetable ripening and development. In some embodiments, altered versions of GCR1 are used to modulate physiol. processes in a plant. The invention further relates to plants comprising constitutively activated non-endogenous GPCRs.

IT 478784-05-3
RL: PRP (Properties)
(unclaimed protein sequence; non-endogenous, constitutively activated plant G protein-coupled receptor GCR1 for modulation of plant development)

RN 478784-05-3 HCAPLUS

CN 24: PN: WO02100882 SEQID: 24 unclaimed protein (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT: 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 12 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2002:173232 HCAPLUS
DOCUMENT NUMBER: 136:396926
TITLE: Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes
INVENTOR(S): Venter, J. Craig; Adams, Mark; Li, Peter W. D.; Myers, Eugene W.
PATENT ASSIGNEE(S): PE Corporation (NY), USA
SOURCE: PCT Int. Appl., 21 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 11
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001071042	A2	20010927	WO 2001-XA9231	20010323 <--
WO 2001071042	A3	20030313		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
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WO 2001071042	A2	20010927	WO 2001-US9231	20010323 <--
WO 2001071042	A3	20030313		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2000-191637P P 20000323
US 2000-614150 A 20000711
WO 2001-US9231 20010323

AB The present invention is based on the sequencing and assembly of the Drosophila melanogaster genome. The present invention provides the primary nucleotide sequence of a large portion of the Drosophila melanogaster genome in a series of genomic and predicted transcript sequences. This information is provided in the form of genomic, transcript and protein sequence information and can be used to generate

nucleic acid detection reagents and kits such as nucleic acid arrays. Primary sequences are provided as contiguous strings in a computer-readable format and recorded on media such as floppy disks, hard disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories. Genes/exons can be predicted,sequences can be edited and homol. searches of target motifs can be conducted. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]

IT 431191-61-6
RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; reagents and kits, such as nucleic acid arrays, for detecting expression of over 10,000 Drosophila genes)

RN 431191-61-6 HCAPLUS

CN Protein (Drosophila melanogaster clone WO0171042-SEQID-5313) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 13 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER:	2002:116544 HCAPLUS
DOCUMENT NUMBER:	136:396996
TITLE:	Human nucleic acids encoding immune/hematopoietic-related proteins
INVENTOR(S):	Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.
PATENT ASSIGNEE(S):	Human Genome Sciences, Inc., USA
SOURCE:	PCT Int. Appl., 3071 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	257
PATENT INFORMATION:	

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001057182	A2	20010809	WO 2001-XC1354	20010117 <--
WO 2001057182	A3	20020328		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2395811	A1	20010802	CA 2001-2395811	20010117 <--
AU 2001041405	A	20010807	AU 2001-41405	20010117 <--
AU 2001041406	A	20010807	AU 2001-41406	20010117 <--
AU 2001041408	A	20010807	AU 2001-41408	20010117 <--
AU 2001041410	A	20010807	AU 2001-41410	20010117 <--
AU 2001041412	A	20010807	AU 2001-41412	20010117 <--
AU 2001041413	A	20010807	AU 2001-41413	20010117 <--
AU 2001041414	A	20010807	AU 2001-41414	20010117 <--
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AU 2001041416	A	20010807	AU 2001-41416	20010117 <--

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AU	2001041418	A	20010807	AU	2001-41418	20010117 <--
AU	2001047190	A	20010807	AU	2001-47190	20010117 <--
AU	2001049053	A	20010807	AU	2001-49053	20010117 <--
AU	2001050767	A	20010807	AU	2001-50767	20010117 <--
AU	2001050768	A	20010807	AU	2001-50768	20010117 <--
AU	2001050769	A	20010807	AU	2001-50769	20010117 <--
AU	2001050770	A	20010807	AU	2001-50770	20010117 <--
WO	2001057182	A2	20010809	WO	2001-US1354	20010117 <--
WO	2001057182	A3	20020328			

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US	20020042096	A1	20020411	US	2001-764887	20010117 <--
US	20020077270	A1	20020620	US	2001-764848	20010117 <--
US	20020086811	A1	20020704	US	2001-764861	20010117 <--
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US	20030092611	A9	20030515			
US	20020086821	A1	20020704	US	2001-764881	20010117 <--
US	20030125246	A9	20030703			
US	20020086822	A1	20020704	US	2001-764886	20010117 <--
US	20030139327	A9	20030724			
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US	20020090615	A1	20020711	US	2001-764878	20010117 <--
US	20020090674	A1	20020711	US	2001-764903	20010117 <--
US	20020094953	A1	20020718	US	2001-764860	20010117 <--
US	20020102638	A1	20020801	US	2001-764846	20010117 <--
US	20020119919	A1	20020829	US	2001-764855	20010117 <--
US	20020132767	A1	20020919	US	2001-764847	20010117 <--
US	20020147140	A1	20021010	US	2001-764877	20010117 <--
US	20020151479	A1	20021017	US	2001-764873	20010117 <--
US	20020161208	A1	20021031	US	2001-764884	20010117 <--
US	20020164685	A1	20021107	US	2001-764857	20010117 <--
US	20020173454	A1	20021121	US	2001-764904	20010117 <--
US	20030044890	A1	20030306	US	2001-764876	20010117 <--
US	20030050231	A1	20030313	US	2001-764872	20010117 <--
AU	2001052878	A	20010807	AU	2001-52878	20010129 <--
AU	2001043137	A	20010814	AU	2001-43137	20010205 <--
AU	2001050771	A	20010820	AU	2001-50771	20010206 <--
AU	2001041411	A	20010820	AU	2001-41411	20010208 <--
US	20030013649	A1	20030116	US	2001-989442	20011121 <--
US	20030054420	A1	20030320	US	2002-72349	20020211 <--
US	20030044904	A1	20030306	US	2002-73865	20020214 <--
US	20030044905	A1	20030306	US	2002-73979	20020214 <--
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US	20030096346	A1	20030522	US	2002-73885	20020214 <--

US 20030039993	A1	20030227	US 2002-79900		20020222 <--
US 20030044907	A1	20030306	US 2002-80110		20020222 <--
US 20030054368	A1	20030320	US 2002-79854		20020222 <--
US 20030039994	A1	20030227	US 2002-91526		20020307 <--
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US 20030054373	A1	20030320	US 2002-91572		20020307 <--
US 20030054375	A1	20030320	US 2002-92154		20020307 <--
US 20030059908	A1	20030327	US 2002-91504		20020307 <--
US 20030068627	A1	20030410	US 2002-91458		20020307 <--
US 20030077606	A1	20030424	US 2002-91438		20020307 <--
US 20030082681	A1	20030501	US 2002-91391		20020307 <--
US 20030054377	A1	20030320	US 2002-102627		20020322 <--
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US 20030054379	A1	20030320	US 2002-116016		20020405 <--
US 20030092615	A1	20030515	US 2002-115928		20020405 <--
US 20030059875	A1	20030327	US 2002-125540		20020419 <--
PRIORITY APPLN. INFO.:			US 2000-179065P	P	20000131
			US 2000-180628P	P	20000204
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			US 2000-198123P	P	20000418
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US 2001-764860	B1	20010117
US 2001-764861	A1	20010117
US 2001-764862	A1	20010117
US 2001-764863	B1	20010117
US 2001-764866	B1	20010117
US 2001-764869	B1	20010117
US 2001-764870	B1	20010117
US 2001-764873	B1	20010117
US 2001-764878	A1	20010117
US 2001-764879	B1	20010117
US 2001-764885	B1	20010117
US 2001-764887	B1	20010117
US 2001-764889	A1	20010117
US 2001-764893	B1	20010117
US 2001-764900	B1	20010117
US 2001-764903	A1	20010117
US 2001-764904	A1	20010117

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention relates to novel immune/hematopoietic-related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "immune/hematopoietic antigens", and the use of such immune/hematopoietic antigens for detecting immune/hematopoietic-related diseases and/or disorders, particularly the presence of cancer and cancer metastases of cells of hematopoietic origin. More specifically, 9752 isolated immune/hematopoietic-associated cDNA and 22,912 genomic DNA mols. are provided that encode novel immune/hematopoietic-associated polypeptides. Novel immune/hematopoietic polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human immune/hematopoietic associated polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the immune system or cells and tissues associated with hematopoiesis, including cancers of cells of hematopoietic origin, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the production and function of the polypeptides of the present invention. [This abstract record is one of twelve records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 428909-41-5P
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human nucleic acids encoding immune/hematopoietic-related proteins)
RN 428909-41-5 HCAPLUS
CN Peptide, (His-Glu-Gln-Glu-Phe-Glu-Thr-Cys-Leu-Asp-Asn-Met-Val-Lys-Pro-Val-Cys-Thr-Lys-Asn-Thr-Lys-Asn-Ser-Trp-Val-Trp-Trp-Arg-Ala-Pro-Cys-Asn-Leu-Ser-Tyr-Leu-Gly-Gly-Xaa-Gly-Arg-Arg-Ile-Ser) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 14 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2001:834397 HCAPLUS
DOCUMENT NUMBER: 136:65028
TITLE: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
AUTHOR(S): Kaneko, Takakazu; Nakamura, Yasukazu; Wolk, C. Peter; Kuritz, Tanya; Sasamoto, Shigemi; Watanabe, Akiko; Iriguchi, Mayumi; Ishikawa, Atsuko; Kawashima, Kumiko; Kimura, Takaharu; Kishida, Yoshie; Kohara, Mitsuyo; Matsumoto, Midori; Matsuno, Ai; Muraki, Akiko; Nakazaki, Naomi; Shimpo, Sayaka; Sugimoto, Masako; Takazawa, Masaki; Yamada, Manabu; Yasuda, Miho; Tabata, Satoshi
CORPORATE SOURCE: Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SOURCE: DNA Research (2001), 8(5), 205-213
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence of the entire genome of a filamentous cyanobacterium, Anabaena sp. strain PCC 7120, was determined The genome of Anabaena consisted of a single chromosome (6,413,771 bp) and six plasmids, designated pCC7120α (408,101 bp), pCC7120β (186,614 bp), pCC7120γ (101,965 bp), pCC7120δ (55,414 bp), pCC7120ε (40,340 bp), and pCC7120ζ (5,584 bp). The chromosome bears 5368 potential protein-encoding genes, four sets of rRNA genes, 48 tRNA genes representing 42 tRNA species, and 4 genes for small structural RNAs. The predicted products of 45% of the potential protein-encoding genes showed sequence similarity to known and predicted proteins of known function, and 27% to translated products of hypothetical genes. The remaining 28% lacked significant similarity to genes for known and predicted proteins in the public DNA databases. More than 60 genes involved in various processes of heterocyst formation and nitrogen fixation were assigned to the chromosome based on their similarity to the reported genes. One hundred and ninety-five genes coding for components of two-component signal transduction systems, nearly 2.5-fold as many as those in Synechocystis sp. PCC 6803, were identified on the chromosome. Only 37% of the Anabaena genes showed significant sequence similarity to those of Synechocystis, indicating a high degree of divergence of the gene information between the two cyanobacterial strains.
IT 374864-24-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete genomic sequence of filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120)
RN 374864-24-1 HCAPLUS
CN Protein (Nostoc sp. PCC 7120 gene alr3304) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT: 379 THERE ARE 379 CAPLUS RECORDS THAT CITE THIS RECORD (380 CITINGS)
REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2001:444843 HCAPLUS
DOCUMENT NUMBER: 135:41840
TITLE: Expressed sequence tags and encoded human proteins
INVENTOR(S): Dumas, Milne Edwards Jean-Baptiste; Jobert, Severin; Giordano, Jean-Yves
PATENT ASSIGNEE(S): Genset, Fr.
SOURCE: Eur. Pat. Appl., 94 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 17
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1104808	A1	20010606	EP 2000-202699	20000727 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1104808	A1	20010606	EP 2000-202699	20000727 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 20070021597	A1	20070125	US 2003-664025	20030915
US 7413875	B2	20080819		
PRIORITY APPLN. INFO.:			US 1999-147499P	P 19990805
			EP 2000-202699	20000727
			US 2000-621976	A3 20000721

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from human mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors. Three hundred sixty 5' ESTs are provided having an incomplete ORF which encodes a signal peptide and 721 have a complete ORF which encodes a signal protein; 955 5'-ESTs are provided having an incomplete ORF in which no signal peptide is identified and 1824 for having a complete ORF in which no signal peptide is identified; and 11,592 5'-ESTs are provided having no open reading frame of 150 nucleotides or larger. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]
IT 343689-56-5P
RL: ANT (Analyte); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); ANST

(Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(amino acid sequence; expressed sequence tags and encoded human proteins)
RN 343689-56-5 HCAPLUS
CN Signal peptide-containing protein (human clone EP1104808-SEQID-5360) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2000:754705 HCAPLUS
DOCUMENT NUMBER: 133:318295
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 46
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225 <--
EP 1033405	A3	20010801		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	A1	20000825	CA 2000-2300692	20000225 <--
EP 1033405	A2	20000906	EP 2000-301439	20000225 <--
EP 1033405	A3	20010801		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1055728	A2	20001129	EP 2000-303770	20000504 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-304161	20000517 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:		
US 1999-121825P	P	19990225
US 1999-145918P	P	19990727
US 1999-145951P	P	19990728
US 1999-146388P	P	19990802
US 1999-146389P	P	19990802
US 1999-146386P	P	19990802
US 1999-147038P	P	19990803
US 1999-147302P	P	19990804
US 1999-147204P	P	19990804
US 1999-147260P	P	19990805
US 1999-147192P	P	19990805
US 1999-147303P	P	19990806
US 1999-147416P	P	19990806
US 1999-147493P	P	19990809

US 1999-147935P	P	19990809
US 1999-148171P	P	19990810
US 1999-148319P	P	19990811
US 1999-148341P	P	19990812
US 1999-148565P	P	19990813
US 1999-148684P	P	19990813
US 1999-149368P		19990816
US 1999-149175P		19990817
US 1999-149426P		19990818
US 1999-149722P		19990820
US 1999-149929P		19990820
US 1999-149723P		19990820
US 1999-149902P		19990823
US 1999-149930P		19990823
US 1999-150566P		19990825
US 1999-150884P		19990826
US 1999-151065P		19990827
US 1999-151066P		19990827
US 1999-151080P		19990827
US 1999-151303P		19990830
US 1999-151438P		19990831
US 1999-151930P		19990901
US 1999-152363P		19990907
US 1999-153070P		19990910
US 1999-153758P		19990913
US 1999-154018P		19990915
US 1999-154039P		19990916
US 1999-154779P		19990920
EP 2000-301439		20000225
US 1999-123180P	P	19990305
US 1999-123548P	P	19990309
US 1999-125788P	P	19990323
US 1999-126264P	P	19990325
US 1999-126785P	P	19990329
US 1999-127462P	P	19990401
US 1999-128234P	P	19990406
US 1999-128714P	P	19990408
US 1999-129845P	P	19990416
US 1999-130077P	P	19990419
US 1999-130449P	P	19990421
US 1999-130510P	P	19990423
US 1999-130891P	P	19990423
US 1999-131449P	P	19990428
US 1999-132048P	P	19990430
US 1999-132407P	P	19990430
US 1999-132484P	P	19990504
US 1999-132485P	P	19990505
US 1999-132486P	P	19990506
US 1999-132487P	P	19990506
US 1999-132863P	P	19990507
US 1999-134256P	P	19990511
US 1999-134218P	P	19990514
US 1999-134219P	P	19990514
US 1999-134221P	P	19990514
US 1999-134370P	P	19990514
US 1999-134768P	P	19990518
US 1999-134941P	P	19990519

US 1999-135124P	P	19990520
US 1999-135353P	P	19990521
US 1999-135629P	P	19990524
US 1999-136021P	P	19990525
US 1999-136392P	P	19990527
US 1999-136782P	P	19990528
US 1999-137222P	P	19990601
US 1999-137528P	P	19990603
US 1999-137502P	P	19990604
US 1999-137724P	P	19990607
US 1999-138094P	P	19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present experiment, but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstract record is one of 15 records supplemental to CA133162185280 necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 133723-30-5, Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) 301865-71-4
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

RN 133723-30-5 HCAPLUS

CN Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 301865-71-4 HCAPLUS

CN Protein (Arabidopsis thaliana clone Ceres_2108050) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER:	2000:754677 HCAPLUS
DOCUMENT NUMBER:	133:318289
TITLE:	Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S):	Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S):	Ceres Inc., USA
SOURCE:	Eur. Pat. Appl., 339 pp. CODEN: EPXXDW
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	46

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225 <--
EP 1033405	A3	20010801		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	A1	20000825	CA 2000-2300692	20000225 <--
EP 1033405	A2	20000906	EP 2000-301439	20000225 <--
EP 1033405	A3	20010801		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1055728	A2	20001129	EP 2000-303770	20000504 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-304161	20000517 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:		
	US 1999-121825P	P 19990225
	US 1999-145918P	P 19990727
	US 1999-145951P	P 19990728
	US 1999-146388P	P 19990802
	US 1999-146389P	P 19990802
	US 1999-146386P	P 19990802
	US 1999-147038P	P 19990803
	US 1999-147302P	P 19990804
	US 1999-147204P	P 19990804
	US 1999-147260P	P 19990805
	US 1999-147192P	P 19990805
	US 1999-147303P	P 19990806
	US 1999-147416P	P 19990806
	US 1999-147493P	P 19990809
	US 1999-147935P	P 19990809
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	US 1999-149426P	19990818
	US 1999-149722P	19990820
	US 1999-149929P	19990820
	US 1999-149723P	19990820
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	US 1999-150884P	19990826
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	US 1999-151303P	19990830
	US 1999-151438P	19990831
	US 1999-151930P	19990901
	US 1999-152363P	19990907
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US 1999-153758P		19990913
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US 1999-154039P		19990916
US 1999-154779P		19990920
EP 2000-301439		20000225
US 1999-123180P	P	19990305
US 1999-123548P	P	19990309
US 1999-125788P	P	19990323
US 1999-126264P	P	19990325
US 1999-126785P	P	19990329
US 1999-127462P	P	19990401
US 1999-128234P	P	19990406
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US 1999-130449P	P	19990421
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US 1999-132407P	P	19990430
US 1999-132484P	P	19990504
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US 1999-134219P	P	19990514
US 1999-134221P	P	19990514
US 1999-134370P	P	19990514
US 1999-134768P	P	19990518
US 1999-134941P	P	19990519
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US 1999-135629P	P	19990524
US 1999-136021P	P	19990525
US 1999-136392P	P	19990527
US 1999-136782P	P	19990528
US 1999-137222P	P	19990601
US 1999-137528P	P	19990603
US 1999-137502P	P	19990604
US 1999-137724P	P	19990607
US 1999-138094P	P	19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present experiment, but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstract record is one of 15 records supplemental to

CA133116218528Q necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT 133723-30-5, Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) 301865-71-4
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)
RN 133723-30-5 HCAPLUS
CN Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 301865-71-4 HCAPLUS
CN Protein (Arabidopsis thaliana clone Ceres_2108050) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 18 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2000:246831 HCAPLUS
DOCUMENT NUMBER: 132:275066
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz De; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland,

Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and

publication system constraints.].
IT 263119-39-7
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)
RN 263119-39-7 HCAPLUS
CN Protein (Drosophila melanogaster gene Sr-CI) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 19 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 2000:9181 HCAPLUS
DOCUMENT NUMBER: 132:89085
TITLE: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
AUTHOR(S): Lin, Xiaoying; Kaul, Samir; Rounsley, Steve; Shea, Terrance P.; Benito, Maria-Lnes; Town, Christopher D.; Fujii, Claire Y.; Mason, Tanya; Bowman, Cheryl L.; Barnstead, Mary; Feldblyum, Tamara V.; Buell, C. Robin; Ketchum, Karen A.; Lee, John; Ronning, Catherine M.; Koo, Hean L.; Moffat, Kelly S.; Cronin, Lisa A.; Shen, Mian; Pai, Grace; Van Aken, Susan; Umayam, Lowell; Tallon, Luke J.; Gill, John E.; Adams, Mark D.; Carrera, Ana J.; Creasy, Todd H.; Goodman, Howard M.; Somerville, Chris R.; Copenhaver, Greg P.; Preuss, Daphne; Nierman, William C.; White, Owen; Eisen, Jonathan A.; Salzberg, Steven L.; Fraser, Claire M.; Venter, J. Craig
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Nature (London) (1999), 402(6763), 760-768
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Arabidopsis thaliana (Arabidopsis) is unique among plant model organisms in having a small genome (130-140 Mb), excellent phys. and genetic maps, and little repetitive DNA. The sequence of chromosome 2 from the Columbia ecotype is reported in two gap-free assemblies (contigs) of 3.6 and 16 megabases (Mb). The latter represents the longest published stretch of uninterrupted DNA sequence assembled from any organism to date. Chromosome 2 represents 15% of the genome and encodes 4037 genes, 49% of which have no predicted function. Roughly 250 tandem gene duplications were found in addition to large-scale duplications of about 0.5 and 4.5 Mb between chromosomes 2 and 1 and between chromosomes 2 and 4, resp. Sequencing of nearly 2 Mb within the genetically defined centromere revealed a low d. of recognizable genes, and a high d. and diverse range of vestigial and presumably inactive mobile elements. More unexpected is what appears to be a recent insertion of a continuous stretch of 75% of the mitochondrial genome into chromosome 2.
IT 133723-30-5, Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence and anal. of chromosome 2 of the plant Arabidopsis thaliana)
RN 133723-30-5 HCAPLUS

CN Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT: 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 1996:132908 HCAPLUS
DOCUMENT NUMBER: 124:196808
ORIGINAL REFERENCE NO.: 124:36259a
TITLE: Class BI and CI scavenger receptors from hamster and Drosophila and the genes encoding them and their therapeutic uses
INVENTOR(S): Krieger, Monty; Acton, Susan L.; Pearson, Alan M.; Rigotti, Attilio
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 84 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
WO 9600288	A2	19960104	WO 1995-US7721	19950619	<--
WO 9600288	A3	19960404			
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TT, UA, US, UZ, VN					
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
US 6429289	B1	20020806	US 1994-265428	19940623	<--
CA 2193832	A1	19960104	CA 1995-2193832	19950619	<--
AU 9528641	A	19960119	AU 1995-28641	19950619	<--
EP 766735	A1	19970409	EP 1995-923943	19950619	<--
EP 766735	B1	20000920			
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE					
JP 10505486	T	19980602	JP 1996-503260	19950619	<--
AT 196503	T	20001015	AT 1995-923943	19950619	<--
US 7078511	B1	20060718	US 1997-765108	19970327	
US 20050136005	A1	20050623	US 2004-933037	20040902	

PRIORITY APPLN. INFO.:
US 1994-265428 A2 19940623
WO 1995-US7721 W 19950619
US 1996-749907 A3 19961115
US 1997-765108 A2 19970327
US 1999-385799 A1 19990830

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB Two distinct scavenger receptors with high affinities for modified lipoproteins and other ligands have been isolated and characterized and cDNAs encoding them cloned. HaSR-BI, and acetylated LDL (AcLDL) and LDL binding scavenger receptor distinct from the type I and type II macrophage scavenger receptors has been isolated and characterized and DNA encoding

the receptor cloned from a variant of Chinese Hampster Ovary Cells, designated Var-261. DSR-CI, a non-mammalian AcLDL binding scavenger receptor having high ligand affinity and broad specificity, was isolated from Drosophila melanogaster. The isolated receptors are useful in screening for drugs that inhibit uptake of cholesterol in endothelial or adipose cells or macrophages, resp. They are also useful as probes for the isolation of other lipoprotein receptors and in research the roles of these receptors. Induction of scavenger receptor synthesis was forced in Var-261 cells by nutritional conditions and an mRNA was cloned by expression in COS cells.

IT 168042-57-7
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; BI and CI scavenger receptors from hamster and Drosophila and genes encoding them and their therapeutic uses)

RN 168042-57-7 HCAPLUS

CN Receptor SR-CI (Drosophila melanogaster scavenger precursor) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 21 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 1995:540739 HCAPLUS

DOCUMENT NUMBER: 123:279210

ORIGINAL REFERENCE NO.: 123:49834h,49835a

TITLE: Expression cloning of dSR-CI, a class C macrophage-specific scavenger receptor from Drosophila melanogaster

AUTHOR(S): Pearson, Alan; Lux, Alison; Krieger, Monty

CORPORATE SOURCE: Dep. Biol., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1995), 92(9), 4056-60
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Mammalian class A macrophage-specific scavenger receptors (SR-A) exhibit unusually broad binding specificity for a wide variety of polyanionic ligands. The properties of these receptors suggest that they may be involved in atherosclerosis and host defense. Previously, a similar receptor activity was observed in Drosophila melanogaster embryonic macrophages and in the Drosophila macrophage-like Schneider L2 cell line. Expression cloning was used to isolate from L2 cells a cDNA that encodes a third class (class C) of scavenger receptor, Drosophila SR-CI (dSR-CI). DSR-CI expression was restricted to macrophages/hemocytes during embryonic development. When expressed in mammalian cells, dSR-CI exhibited high affinity and saturable binding of 125I-labeled acetylated low-d. lipoprotein and mediated its chloroquine-dependent, presumably lysosomal, degradation Although the broad polyanionic ligand-binding specificity of dSR-CI was similar to that of SR-A, their predicted protein sequences are not similar. DSR-CI is a 609-residue type I integral membrane protein

containing several well-known sequence motifs, including 2 complement control protein (CCP) domains and somatomedin B, MAM, and mucin-like domains. Macrophage scavenger receptors apparently mediate important, well-conserved functions and may be pattern-recognition receptors that arose early in the evolution of host-defense mechanisms. Genetic and physiol. anal. of dSR-CI function in Drosophila should provide further insights into the roles played by scavenger receptors in host defense and development.

IT 168042-57-7
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; expression cloning of dSR-CI, a class C macrophage-specific scavenger receptor from Drosophila melanogaster)

RN 168042-57-7 HCAPLUS

CN Receptor SR-CI (Drosophila melanogaster scavenger precursor) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 156 THERE ARE 156 CAPLUS RECORDS THAT CITE THIS RECORD (156 CITINGS)

L3 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER:	1994:429903 HCAPLUS
DOCUMENT NUMBER:	121:29903
ORIGINAL REFERENCE NO.:	121:5441a,5444a
TITLE:	Cellulase variants and their use in washing compositions
INVENTOR(S):	Schulein, Martin; Fredholm, Henrik; Hjort, Carsten Mailand; Rasmussen, Grethe; Nielsen, Egon; Rosholm, Peter
PATENT ASSIGNEE(S):	Novo Nordisk A/S, Den.
SOURCE:	PCT Int. Appl., 82 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9407998	A1	19940414	WO 1993-DK327	19931006 <--
W: BR, FI, JP, KR, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 663950	A1	19950726	EP 1993-922899	19931006 <--
EP 663950	B1	20040317		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 08501692	T	19960227	JP 1994-508604	19931006 <--
JP 3681750	B2	20050810		
BR 9307198	A	19990330	BR 1993-7198	19931006 <--
AT 262035	T	20040415	AT 1993-922899	19931006
EP 1431389	A2	20040623	EP 2004-6060	19931006
EP 1431389	A3	20040630		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
FI 9501629	A	19950405	FI 1995-1629	19950405 <--
US 5792641	A	19980811	US 1995-411777	19950505 <--
US 6114296	A	20000905	US 1998-57088	19980408 <--
PRIORITY APPLN. INFO.:			DK 1992-1221 A	19921006

DK 1992-1222	A	19921006
DK 1992-1223	A	19921006
DK 1992-1224	A	19921006
DK 1992-1225	A	19921006
DK 1992-1513	A	19921218
DK 1992-1515	A	19921218
DK 1992-1543	A	19921223
EP 1993-922899	A3	19931006
WO 1993-DK327	W	19931006

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB A cellulase variant of a parent cellulase, e.g. a cellulase classified in family 45 such as a Humicola insolens 43 kD endoglucanase, comprising a cellulose binding domain (CBD), a catalytically active domain (CAD) and a region linking the cellulose binding domain and catalytically active domain (the linking region), wherein one more amino acid residues of the CBD, CAD or linking region is deleted or substituted by one or more amino acid residues and/or one or more amino acids are added to the linking region and/or another CBD is added at the opposite end of the catalytically active domain is described. These variants have improved properties as regards to, e.g., alkaline activity, compatibility with detergent composition ingredients, particulate soil removal, color clarification, defuzzing, depilling, harshness reduction, and sensitivity to anionic surfactants and peroxidase bleaching systems. The variants are in detergent compns., for textile treatment, in paper pulp processing, for animal feed and for stone washing of jeans. Variants of Humicola insolens endoglucanase were prepared by site-specific mutagenesis of the gene and expression of the mutant in Aspergillus oryzae. Resistance to peroxidase and anionic surfactants and improved washing ability were demonstrated using these variants.

IT 156067-92-4, [Glu-265]endoglucanase (Humicola insolens)
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, for use in washing compns.)

RN 156067-92-4 HCAPLUS

CN Cellulase (Humicola insolens strain DSM 1800 reduced), 265-L-glutamic acid- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 1994:1856 HCAPLUS

DOCUMENT NUMBER: 120:1856

ORIGINAL REFERENCE NO.: 120:455a,458a

TITLE: Cloning, nucleotide sequence and expression in Escherichia coli of a gene (ompM) encoding a 25 kDa major outer-membrane protein (MOMP) of Legionella pneumophila

AUTHOR(S): High, Andrea S.; Torosian, Steven D.; Rodgers, Frank G.

CORPORATE SOURCE: Dep. Microbiol., Univ. New Hampshire, Durham, NH, 03824-3544, USA

SOURCE: Journal of General Microbiology (1993), 139(8), 1715-21
CODEN: JGMIAN; ISSN: 0022-1287

DOCUMENT TYPE: Journal
LANGUAGE: English
AB A genomic library derived from a virulent isolate of Legionella pneumophila was constructed in Escherichia coli JM 83 using the cloning vector pUC19. The clones were screened by filter immunoassay using L. pneumophila rabbit polyclonal antisera and in the absence of in situ bacterial lysis one such clone, LP 116, expressed L. pneumophila-specific antigens on the surface of E. coli. Restriction endonuclease digest anal. and agarose gel electrophoresis revealed a fragment measuring approx. 750 bp. Southern hybridization confirmed that the fragment was L. pneumophila DNA. Sequencing data showed that the fragment was 810 bp in length with an open reading frame (ORF) of 678 bp. The outer-membrane profiles of the E. coli parent, the L. pneumophila DNA-contributing strain and clone LP 116 were compared by SDS-PAGE. A protein of 25 kDa was found in outermembrane prepns. of both the clone LP 116 and L. pneumophila but not in E. coli JM 83. This was in agreement with the mol. mass of the deduced peptide of the mature protein. Immunoblots using L. pneumophila-specific polyclonal antiserum confirmed that this 25 kDa outer-membrane protein (OMP) was a L. pneumophila polypeptide. Both direct immunofluorescence assay and immunoblots using the com. produced monoclonal antibody specific for the common antigen of the major outer-membrane protein (MOMP) confirmed that the 25 kDa protein produced by LP 116 was involved with the MOMP complex. The gene encoding this protein has been designated ompM. Furthermore, using the fertile chicken egg virulence assay, clone LP 116 producing the 25 kDa MOMP of L. pneumophila showed an increase in virulence when compared to the E. coli parent strain.
IT 151689-51-9, 25 KDa major outer membrane protein (Legionella pneumophila clone LP 116 gene ompM)
RL: PRP (Properties)
(amino acid sequence and expression in Escherichia coli of)
RN 151689-51-9 HCAPLUS
CN Protein (Legionella pneumophila clone LP116 gene ompM outer membrane reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT: 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L3 ANSWER 24 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER: 1991:200647 HCAPLUS
DOCUMENT NUMBER: 114:200647
ORIGINAL REFERENCE NO.: 114:33693a,33696a
TITLE: Molecular cloning and characterization of GPA1, a G protein α subunit gene from Arabidopsis thaliana
AUTHOR(S): Ma, Hong; Yanofsky, Martin F.; Meyerowitz, Elliot M.
CORPORATE SOURCE: Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1990), 87(10), 3821-5
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A gene coding for a G protein α subunit from the flowering plant A. thaliana was isolated. This gene, named GPA1, was isolated by using a DNA probe generated by polymerase chain reaction based on protein sequences from mammalian and yeast G protein α subunits. The sequences of genomic and cDNA clones indicate that GPA1 has 14 exons, and the deduced

amino acid sequence shows that the GPA1 gene product (GPα1) has 383 amino acid residues (44,582 Da). The GPα1 protein exhibits similarity to all known G protein α subunits; 36 of its amino acids are identical and 73 are similar (identical and conservative changes) to mammalian inhibitory guanine nucleotide-binding regulatory factor α subunits and transducins. Further, the GPα1 protein has all of the consensus regions for a GTP-binding protein. The GPA1-encoded mRNA of 1.55 kilobases is most abundant in vegetative plant tissues, as determined by RNA blot anal. Restriction fragment length polymorphism mapping expts. show that GPA1 is .apprx.1.2 centimorgans from the visible marker er on chromosome 2.

IT 133723-30-5, Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced)
RL: PRP (Properties)
(amino acid sequence of)

RN 133723-30-5 HCAPLUS

CN Protein G (Arabidopsis thaliana clone pCIT1828 guanine nucleotide-binding α-subunit reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

OS.CITING REF COUNT: 120 THERE ARE 120 CAPLUS RECORDS THAT CITE THIS RECORD (120 CITINGS)

L3 ANSWER 25 OF 26 HCAPLUS COPYRIGHT 2011 ACS on STN

ACCESSION NUMBER: 1991:159271 HCAPLUS

DOCUMENT NUMBER: 114:159271

ORIGINAL REFERENCE NO.: 114:26811a,26814a

TITLE: Primary structure of two linker chains of the extracellular hemoglobin from the polychaete Tylorrhynchus heterochaetus

AUTHOR(S): Suzuki, Tomohiko; Takagi, Takashi; Gotoh, Toshio

CORPORATE SOURCE: Fac. Sci., Kochi Univ., Kochi, 780, Japan

SOURCE: Journal of Biological Chemistry (1990), 265(21), 12168-77
CODEN: JBCHA3; ISSN: 0021-9258

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Two types of linker subunits (linkers 1 and 2) of the extracellular Hb of T. heterochaetus were isolated as disulfide-linked homodimers by C18 reverse-phase chromatog. These subunits constituted 6 and 13%, resp., of total protein area on the chromatogram. The complete amino acid sequences of linkers 1 and 2 were determined by automated Edman sequencing of the peptides derived by digestions with lysyl endopeptidase, trypsin, chymotrypsin, Staphylococcus aureus V8 protease, pepsin, and endoproteinase Asp-N. The linker 1 consisted of 253 amino acid residues (mol. weight = 28,200), whereas the linker 2 consisted of 236 residues (mol. weight = 26,316). The 2 chains showed 27% sequence identity. The amino acid sequences of Tylorrhynchus linkers 1 and 2 also showed 23-27% homol. with the recently determined sequence of a linker chain of Lamellibrachia Hb. In the 3 linker chains, half-cystine residues were highly conserved; 8 out of 13 residues were identical, suggesting that such residues would contribute to the formation of intrachain disulfide bonds essential for the protein folding of the linker polypeptides. Based on the exact mol. wts. of the linker and the heme-containing subunits, the molar ratios estimated for the subunits and the min. mol. wts. per 1 mol of heme, a model was proposed for the subunit structure of the Tylorrhynchus Hb, consisting of 216 polypeptide chains, 192 heme-containing chains, and 24 linker chains.

```
IT   133064-30-9, Hemoglobin (Tylorrhynchus heterochaetus linker
     chain 1 reduced)
     RL: PRP (Properties)
        (amino acid sequence of)
RN   133064-30-9  HCAPLUS
CN   Hemoglobin (Tylorrhynchus heterochaetus linker chain 1 reduced) (9CI)  (CA
     INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT:     15     THERE ARE 15 CAPLUS RECORDS THAT CITE THIS
                                RECORD (15 CITINGS)

L3   ANSWER 26 OF 26  HCAPLUS  COPYRIGHT 2011 ACS on STN
ACCESSION NUMBER:         1989:529229  HCAPLUS
DOCUMENT NUMBER:          111:129229
ORIGINAL REFERENCE NO.:   111:21527a,21530a
TITLE:                    Amino acid sequence of a long-chain neurotoxin
                          homolog, Pa ID, from the venom of an Australian elapid
                          snake, Pseudechis australis
AUTHOR(S):                Takasaki, Chikahisa
CORPORATE SOURCE:         Fac. Sci., Tohoku Univ., Sendai, 980, Japan
SOURCE:                   Journal of Biochemistry (1989), 106(1), 11-16
                          CODEN: JOBIAO; ISSN: 0021-924X
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   Pa ID, a long-chain neurotoxin homolog, was isolated from the venom of an
     Australian elapid snake, P. australis, and its amino acid sequence was
     determined by conventional methods.  Pa ID was an acidic protein (pI = 6.2) and
     consisted of 68 amino acid residues.  It did not show binding activity to
     the acetylcholine receptor of an elec. ray (Marke japonica) nor lethal
     effect on mice, though the amino acid sequence is homologous with those of
     long-chain neurotoxins isolated from other elapid snakes (homol., 39-51%).
     In the sequence of Pa ID, a structurally invariant residue (tyrosine-22)
     and 2 functionally invariant residues [valine-alanine(Ala)-49 and
     lysine/arginine(Arg)-50] in snake venom neurotoxins are replaced by a
     cysteine, an Arg, and a methionine residue, resp., and furthermore, 4
     common residues in long-chain neurotoxins, glycine-17, Ala-43, serine-59,
     and phenylalanine/histidine-66 are replaced by a glutamic acid, a
     threonine (Thr), a Thr, and a valine residue, resp.  The conformational
     change of the protein mol. caused by these replacements and the removal of
     a pos. charge at position 50 are probably the reasons why Pa ID has lost
     the lethality.
IT   122633-67-4, Neurotoxin Pa-ID (Pseudechis australis reduced)
     RL: PRP (Properties)
        (amino acid sequence of)
RN   122633-67-4  HCAPLUS
CN   Neurotoxin Pa-ID (Pseudechis australis reduced) (9CI)  (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
OS.CITING REF COUNT:     5     THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD
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     FILE 'HCAPLUS' ENTERED AT 11:43:29 ON 17 MAR 2011
L2           65 SEA ABB=ON  PLU=ON  L1
L3           26 SEA ABB=ON  PLU=ON  L2 AND (PD<20031115)
                D L3 IBIB ABS HITSTR 1-26


     FILE HOME

     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
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     STRUCTURE FILE UPDATES:   16 MAR 2011  HIGHEST RN 1268669-05-1
     DICTIONARY FILE UPDATES:  16 MAR 2011  HIGHEST RN 1268669-05-1

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     http://www.cas.org/support/stngen/stndoc/properties.html

     FILE HCAPLUS

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     FILE COVERS 1907 - 17 Mar 2011  VOL 154 ISS 12
     FILE LAST UPDATED: 16 Mar 2011  (20110316/ED)
     REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Dec 2010
     USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Dec 2010

     HCAplus now includes complete International Patent Classification (IPC)
     reclassification data for the fourth quarter of 2010.

     CAS Information Use Policies apply and are available at:

     http://www.cas.org/legal/infopolicy.html
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     This file contains CAS Registry Numbers for easy and accurate
     substance identification.

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L1          161 SEA FILE=REGISTRY ABB=ON  PLU=ON  ETC.{4,20}CTK/SQSP
L2           65 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1
L3           26 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L2 AND (PD<20031115)


=> D HIS FULL

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     FILE 'REGISTRY' ENTERED AT 11:40:44 ON 17 MAR 2011
L1          161 SEA ABB=ON  PLU=ON  ETC.{4,20}CTK/SQSP

     FILE 'HCAPLUS' ENTERED AT 11:43:29 ON 17 MAR 2011
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                D QUE STAT


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     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:   16 MAR 2011  HIGHEST RN 1268669-05-1
     DICTIONARY FILE UPDATES:  16 MAR 2011  HIGHEST RN 1268669-05-1

     CAS Information Use Policies apply and are available at:

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       Please note that search-term pricing does apply when
       conducting SmartSELECT searches.

     REGISTRY includes numerically searchable data for experimental and
     predicted properties as well as tags indicating availability of
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     http://www.cas.org/support/stngen/stndoc/properties.html

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FILE COVERS 1907 - 17 Mar 2011 VOL 154 ISS 12
FILE LAST UPDATED: 16 Mar 2011 (20110316/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2010
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2010

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-22.62	-22.62

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